



CATS-5002-C1 Substitute Seq List.ST25
SEQUENCE LISTING

<110> TAKEDA SAN DIEGO, INC.
<120> CRYSTALLIZATION OF CATHEPSIN S
<130> CATS-5002-C1
<140> 10/646,470
<141> 2003-08-22
<150> US 60/405,423
<151> 2002-08-23
<160> 4
<170> PatentIn version 3.3
<210> 1
<211> 331
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<222> (1)..(331)
<223> Amino acid sequence for full-length human wild type Cathepsin S

<300>
<308> AF230097
<309> 2002-04-08
<313> (1)..(331)

<400> 1
Met Lys Arg Leu Val Cys Val Leu Leu Val Cys Ser Ser Ala Val Ala
1 5 10 15
Gln Leu His Lys Asp Pro Thr Leu Asp His His Trp His Leu Trp Lys
20 25 30
Lys Thr Tyr Gly Lys Gln Tyr Lys Glu Lys Asn Glu Glu Ala Val Arg
35 40 45
Arg Leu Ile Trp Glu Lys Asn Leu Lys Phe Val Met Leu His Asn Leu
50 55 60
Glu His Ser Met Gly Met His Ser Tyr Asp Leu Gly Met Asn His Leu
65 70 75 80
Gly Asp Met Thr Ser Glu Glu Val Met Ser Leu Met Ser Ser Leu Arg
85 90 95
Val Pro Ser Gln Trp Gln Arg Asn Ile Thr Tyr Lys Ser Asn Pro Asn
100 105 110

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Arg Ile Leu Pro Asp Ser Val Asp Trp Arg Glu Lys Gly Cys Val Thr
115 120 125

Glu Val Lys Tyr Gln Gly Ser Cys Gly Ala Cys Trp Ala Phe Ser Ala
130 135 140

Val Gly Ala Leu Glu Ala Gln Leu Lys Leu Lys Thr Gly Lys Leu Val
145 150 155 160

Ser Leu Ser Ala Gln Asn Leu Val Asp Cys Ser Thr Glu Lys Tyr Gly
165 170 175

Asn Lys Gly Cys Asn Gly Gly Phe Met Thr Thr Ala Phe Gln Tyr Ile
180 185 190

Ile Asp Asn Lys Gly Ile Asp Ser Asp Ala Ser Tyr Pro Tyr Lys Ala
195 200 205

Met Asp Leu Lys Cys Gln Tyr Asp Ser Lys Tyr Arg Ala Ala Thr Cys
210 215 220

Ser Lys Tyr Thr Glu Leu Pro Tyr Gly Arg Glu Asp Val Leu Lys Glu
225 230 235 240

Ala Val Ala Asn Lys Gly Pro Val Ser Val Gly Val Asp Ala Arg His
245 250 255

Pro Ser Phe Phe Leu Tyr Arg Ser Gly Val Tyr Tyr Glu Pro Ser Cys
260 265 270

Thr Gln Asn Val Asn His Gly Val Leu Val Val Gly Tyr Gly Asp Leu
275 280 285

Asn Gly Lys Glu Tyr Trp Leu Val Lys Asn Ser Trp Gly His Asn Phe
290 295 300

Gly Glu Glu Gly Tyr Ile Arg Met Ala Arg Asn Lys Gly Asn His Cys
305 310 315 320

Gly Ile Ala Ser Phe Pro Ser Tyr Pro Glu Ile
325 330

<210> 2
<211> 996
<212> DNA
<213> Homo sapiens

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<220>
 <221> misc_feature
 <222> (1)..(996)
 <223> Human cDNA sequence for Cathepsin S

<400> 2
 atgaaacggc tggtttgtgt gctcttggtg tgctcctctg cagtggcaca gttgcataaa 60
 gatcctaccc tggatcacca ctggcatctc tgggaagaaaa cctatggcaa acaataacaag 120
 gaaaagaatg aagaagcagt acgacgtctc atctgggaaa agaatctaaa gtttgtgatg 180
 cttcacaacc tggagcattc aatgggaatg cactcatacg atctgggcat gaaccacctg 240
 ggagacatga ccagtgaaga agtgatgtct ttgatgagtt ccctgagagt tcccagccag 300
 tggcagagaa atatcacata taagtcaaac cctaatacga tattgcctga ttctgtggac 360
 tggagagaga aaggggtgtg tactgaagtg aaatatcaag gttcttgtgg tgcttgctgg 420
 gctttcagtg ctgtgggggc cctggaagca cagctgaagc tgaaaacagg aaagctggtg 480
 tctctcagtg cccagaacct ggtggattgc tcaactgaaa aatatggaaa caaaggctgc 540
 aatggtggct tcatgacaac ggctttccag tacatcattg ataacaaggg catcgactca 600
 gacgcttcct atccctacaa agccatggat ctgaaatgtc aatatgactc aaaatatcgt 660
 gctgccacat gttcaaagta cactgaactt ccttatggca gagaagatgt cctgaaagaa 720
 gctgtggcca ataaaggccc agtgtctgtt ggtgtagatg cgcgtcatcc ttctttcttc 780
 ctctacagaa gtggtgtcta ctatgaacca tcctgtactc agaatgtgaa tcatggtgta 840
 cttgtggttg gctatggtga tcttaatggg aaagaatact ggcttgtgaa aaacagctgg 900
 ggccacaact ttggtgaaga aggatattatt cggatggcaa gaaataaagg aaatcattgt 960
 gggattgcta gctttccctc ttaccacagaa atctag 996

<210> 3
 <211> 225
 <212> PRT
 <213> Artificial

<220>
 <223> Amino acid sequence for residues 114-331 of Cathepsin S with a C-terminal Glycine-6x-histidine tag

<220>
 <221> MISC_FEATURE
 <222> (1)..(218)
 <223> Amino acid sequence for residues 114-331 of Cathepsin S

<220>
 <221> MISC_FEATURE
 <222> (219)..(225)
 <223> Amino acid sequence for C-terminal Glycine-6x-histidine tag

<400> 3

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Ile Leu Pro Asp Ser Val Asp Trp Arg Glu Lys Gly Cys Val Thr Glu
1 5 10 15

Val Lys Tyr Gln Gly Ser Cys Gly Ala Cys Trp Ala Phe Ser Ala Val
20 25 30

Gly Ala Leu Glu Ala Gln Leu Lys Leu Lys Thr Gly Lys Leu Val Ser
35 40 45

Leu Ser Ala Gln Asn Leu Val Asp Cys Ser Thr Glu Lys Tyr Gly Asn
50 55 60

Lys Gly Cys Asn Gly Gly Phe Met Thr Thr Ala Phe Gln Tyr Ile Ile
65 70 75 80

Asp Asn Lys Gly Ile Asp Ser Asp Ala Ser Tyr Pro Tyr Lys Ala Met
85 90 95

Asp Gln Lys Cys Gln Tyr Asp Ser Lys Tyr Arg Ala Ala Thr Cys Ser
100 105 110

Lys Tyr Thr Glu Leu Pro Tyr Gly Arg Glu Asp Val Leu Lys Glu Ala
115 120 125

Val Ala Asn Lys Gly Pro Val Ser Val Gly Val Asp Ala Arg His Pro
130 135 140

Ser Phe Phe Leu Tyr Arg Ser Gly Val Tyr Tyr Glu Pro Ser Cys Thr
145 150 155 160

Gln Asn Val Asn His Gly Val Leu Val Val Gly Tyr Gly Asp Leu Asn
165 170 175

Gly Lys Glu Tyr Trp Leu Val Lys Asn Ser Trp Gly His Asn Phe Gly
180 185 190

Glu Glu Gly Tyr Ile Arg Met Ala Arg Asn Lys Gly Asn His Cys Gly
195 200 205

Ile Ala Ser Phe Pro Ser Tyr Pro Glu Ile Gly His His His His His
210 215 220

His
225

<210> 4
<211> 340
<212> PRT

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<213> Artificial

<220>

<223> Amino acid sequence for Cathepsin S with an N-terminal Methionine-Proline and a C-terminal Glycine-6x-histidine tag

<220>

<221> MISC_FEATURE

<222> (1)..(2)

<223> Amino acid sequence for an N-terminal Methionine-Proline tag

<220>

<221> MISC_FEATURE

<222> (3)..(333)

<223> Amino acid sequence for Cathepsin S

<220>

<221> MISC_FEATURE

<222> (334)..(340)

<223> Amino acid sequence for a C-terminal Glycine-6x-histidine tag

<400> 4

Met Pro Met Lys Arg Leu Val Cys Val Leu Leu Val Cys Ser Ser Ala
1 5 10 15

Val Ala Gln Leu His Lys Asp Pro Thr Leu Asp His His Trp His Leu
20 25 30

Trp Lys Lys Thr Tyr Gly Lys Gln Tyr Lys Glu Lys Asn Glu Glu Ala
35 40 45

Val Arg Arg Leu Ile Trp Glu Lys Asn Leu Lys Phe Val Met Leu His
50 55 60

Asn Leu Glu His Ser Met Gly Met His Ser Tyr Asp Leu Gly Met Asn
65 70 75 80

His Leu Gly Asp Met Thr Ser Glu Glu Val Met Ser Leu Met Ser Ser
85 90 95

Leu Arg Val Pro Ser Gln Trp Gln Arg Asn Ile Thr Tyr Lys Ser Asn
100 105 110

Pro Asn Arg Ile Leu Pro Asp Ser Val Asp Trp Arg Glu Lys Gly Cys
115 120 125

Val Thr Glu Val Lys Tyr Gln Gly Ser Cys Gly Ala Cys Trp Ala Phe
130 135 140

Ser Ala Val Gly Ala Leu Glu Ala Gln Leu Lys Leu Lys Thr Gly Lys
145 150 155 160

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Leu Val Ser Leu Ser Ala Gln Asn Leu Val Asp Cys Ser Thr Glu Lys
 165 170 175
 Tyr Gly Asn Lys Gly Cys Asn Gly Gly Phe Met Thr Thr Ala Phe Gln
 180 185 190
 Tyr Ile Ile Asp Asn Lys Gly Ile Asp Ser Asp Ala Ser Tyr Pro Tyr
 195 200 205
 Lys Ala Met Asp Gln Lys Cys Gln Tyr Asp Ser Lys Tyr Arg Ala Ala
 210 215 220
 Thr Cys Ser Lys Tyr Thr Glu Leu Pro Tyr Gly Arg Glu Asp Val Leu
 225 230 235 240
 Lys Glu Ala Val Ala Asn Lys Gly Pro Val Ser Val Gly Val Asp Ala
 245 250 255
 Arg His Pro Ser Phe Phe Leu Tyr Arg Ser Gly Val Tyr Tyr Glu Pro
 260 265 270
 Ser Cys Thr Gln Asn Val Asn His Gly Val Leu Val Val Gly Tyr Gly
 275 280 285
 Asp Leu Asn Gly Lys Glu Tyr Trp Leu Val Lys Asn Ser Trp Gly His
 290 295 300
 Asn Phe Gly Glu Glu Gly Tyr Ile Arg Met Ala Arg Asn Lys Gly Asn
 305 310 315 320
 His Cys Gly Ile Ala Ser Phe Pro Ser Tyr Pro Glu Ile Gly His His
 325 330 335
 His His His His
 340